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WHAT IS CLAIMED IS:

1                   1.       A method of controlling cancer suppression in a mammal having a  
 2 cancer suppressing gene, comprising the steps of:  
 3                   making a substantially duplicated genetic material corresponding to the  
 4 genetic material of said gene, the substantially duplicated material selected from the group  
 5 consisting of a cloned cancer suppressing gene, a modified or defective cancer suppressing  
 6 gene, homologues thereof, fragments thereof, and mixtures thereof; and  
 7                   interchanging said duplicated genetic material and the cancer suppressing gene  
 8 of the mammal.

1                   2.       A method of claim 1, wherein before said making a substantially  
 2 duplicated genetic material, determining the chromosomal location of said cancer suppressing  
 3 gene of the mammal.

1                   3.       A method of claim 1, wherein after said making a substantially  
 2 duplicated genetic material, detecting the presence or absence of an inactive cancer  
 3 suppressing gene of a tissue sample of the mammal to determine whether or not the tissue  
 4 sample cancer suppressing gene is defective or absent.

1                   4.       A method of claim 3, wherein in response to a determination that the  
 2 tissue sample cancer suppressing gene is either defective or absent, replacing a cancer  
 3 suppressing gene of the mammal with its clone.

1                   5.       A method of claim 3, wherein the determination of whether or not the  
 2 tissue sample cancer suppressing gene is defective or absent is accomplished by measuring  
 3 the amount of protein product of said cancer suppressing gene, of the tissue sample, bound by  
 4 an antibody specific for said protein.

1                   6.       A method of claim 5, wherein the determination of whether or not the  
 2 tissue sample cancer suppressing gene is defective or absent is accomplished by:

- 3                   (a)       labeling said tissue sample with radioactive isotope;
- 4                   (b)       lysing the labeled tissue;
- 5                   (c)       reacting the protein product of said cancer suppressing gene with an
- 6 antibody specific for said protein thereby forming a protein/antibody immunocomplex;
- 7                   (d)       autoradiographing the immunocomplex obtained in step (c); and

8 (e) determining the presence or absence of the protein product by  
9 comparing the autoradiogram of step (d) with the autoradiogram of the standard protein  
10 product.

1 7. The method of claim 5, wherein the determination of whether or not  
2 the tissue sample cancer suppressing gene is defective or absent is accomplished by enzyme  
3 immunoassay techniques.

1 8. The method of claim 5, wherein the determination of whether or not  
2 the tissue sample cancer suppressing gene is defective or absent is accomplished by  
3 immunocytochemistry methods.

1 9. The method of claim 5, wherein the cancer suppressing gene is the RB  
2 gene and the protein product is ppRB<sup>110</sup>.

1 10. The method of claim 1, wherein said cancer suppressing gene is  
2 replaced with substantially duplicated material selected from the group consisting of said  
3 cloned cancer suppressing gene, homologues thereof, fragments thereof, and mixtures  
4 thereof, for therapeutic purposes.

1 11. The method of claim 1, wherein said cancer suppressing gene is  
2 replaced with substantially duplicated material selected from the group consisting of said  
3 defective cancer suppressing gene, homologues thereof, fragments thereof, and mixtures  
4 thereof, for facilitating the testing of the carcinogenicity of environmental influences.

1 12. The method of claim 2, wherein the location of said cancer suppressing  
2 gene is determined by chromosome walking.

1 13. The method of claim 2, wherein the location of said cancer suppressing  
2 gene is determined through organic markers.

1 14. A method of claim 2, wherein:  
2 said chromosomal location of said cancer suppressing gene is determined by  
3 testing genes of a chromosome for phenotypic expression;  
4 determining one of the genes of said chromosome to be a marker gene; and  
5 using chromosomal walking techniques to locate a cancer suppressing gene.

1           15.     An animal genetically altered so as to have the allele of at least one  
2 cancer suppressing gene selected from the group consisting of a defective allele, a homologue  
3 thereof, a fragment thereof, and a mixture thereof.

1           16.     An animal of claim 15, wherein said defective allele is selected from  
2 the group consisting of defective alleles of RB genes, breast cancer suppressing genes,  
3 Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes,  
4 bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes,  
5 small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes,  
6 acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, homologues  
7 thereof, fragments thereof, and mixtures thereof.

1           17.     An animal of claim 15, wherein said allele contains a DNA fragment  
2 having at least one defective nucleotide sequence.

1           18.     An animal of claim 15, wherein said defective allele contains a DNA  
2 fragment having at least one defective RB nucleotide sequence.

1           19.     The animal of claim 15, wherein said animal is a mouse.

1           20.     A method for determining the carcinogenicity of suspected  
2 environmental influences, using the animal of claim 14, comprising the steps of:  
3                exposing said animal to a suspected environmental influence;  
4                observing the animal for the phenotypic expression of cancer; and  
5                determining carcinogenicity of the suspected environmental influence in  
6 response to observing a phenotypic expression of cancer in the animal.

1           21.     A method of claim 20, wherein said exposing includes exposing to a  
2 source of radiation.

1           22.     A method of claim 20, wherein said exposing includes exposing to  
2 tobacco combustion products.

1           23.     A method of claim 20, wherein said exposing includes exposing to  
2 food additives.

1                   24.     A method of claim 20, wherein said exposing includes exposing to  
2     artificial substances.

1                   25.     A method of claim 20, wherein said observing includes examining the  
2     animal for tumor development.

1                   26.     A method of claim 25, wherein in response to the formation of a tumor  
2     in the animal, analyzing the tumor for the presence of cancer cells.

1                   27.     A method of making the animal of claim 15, comprising:  
2                   using at least one allele of an animal cancer suppressing gene selected from  
3     the group consisting of a defective allele, a homologue thereof, a fragment thereof, and a  
4     mixture thereof;  
5                   mutating at least one animal cell with said allele to form a mutated cell;  
6                   introducing said mutated cell into an animal blastocyst;  
7                   permitting growth of the blastocyst for a given period of time sufficient to  
8     incorporate said allele into its cells; repressing genetic recombinations within said cells;  
9     transferring the blastocyst containing said allele into the uterus of a pseudo pregnant animal  
10    for giving birth subsequently to an animal bearing said allele;  
11                  breeding said animal to reproduce additional animals; and  
12                  selecting the animal of claim 14 from said additional animals by determining  
13    the presence therein of the said allele.

1                   28.     A method of claim 27, wherein before introducing said allele,  
2     removing said blastocyst from a super ovulated animal, and wherein said blastocyst is  
3     comprised of undifferentiated cells.

1                   29.     A method of claim 27, wherein said introducing is performed in vitro.

1                   30.     A pharmaceutical composition wherein the active ingredient is selected  
2     from the group consisting of a naturally occurring intact cancer suppressing gene, a cloned  
3     intact cancer suppressing gene, fragments thereof, homologues thereof and mixtures thereof.

1                   31.     A pharmaceutical composition of claim 30, wherein said naturally  
2     occurring and cloned cancer suppressing gene is selected from the group consisting of RB  
3     genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-

Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, homologues thereof, fragments thereof, and mixtures thereof.

32. A pharmaceutical composition of claim 30, wherein the active ingredient is selected from the group consisting of RB cDNA, modified RB cDNA fragment, clones thereof, homologues thereof and mixtures thereof.

33. A pharmaceutical composition of claim 31, wherein the active ingredient for each of said gene is selected from the group consisting of cDNA of said gene, fragments of said cDNA, homologues thereof and mixtures thereof.

34. A pharmaceutical composition of claim 32, wherein the cancer suppressing gene is isolated from human chromosome 13 region 13q14.

35. A pharmaceutical composition of claim 31, wherein the cancer suppressing gene and its clone each has the following nucleotide sequence:

TTCCGGTTTT	TCTCAGGGGA	CGTTGAAATT	ATTTTTGTAA	CGGGAGTCGG	GAGAGGACGG	60										
GGCGTGCCCC	GCGTGCGCGC	GCGTCGTCCT	CCCCGGCGCT	CCTCCACAGC	TCGCTGGCTC	120										
CCGCCGCGGA	AAGGCGTC	ATG	CCG	CCC	AAA	ACC	CCC	CGA	AAA	ACG	GCC	GCC	171			
		Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala				
		1				5					10					
ACC	GCC	GCC	GCT	GCC	GCC	GCG	GAA	CCC	CCG	GCA	CCG	CCG	CCG	CCG	CCC	219
Thr	Ala	Ala	Ala	Ala	Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	
			15				20				25					
CCT	CCG	TAG	GAG	GAC	CCA	GAG	CAG	GAC	AGC	GGC	CCG	GAG	GAC	CTG	CCT	267
Pro	Pro	Glu	Glu	Asp	Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	
		30				35					40					
CTC	GTC	AGG	CTT	GAG	TTT	GAA	GAA	ACA	GAA	GAA	CCT	GAT	TTT	ACT	GCA	315
Leu	Val	Arg	Leu	Glu	Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	
	45					50					55					
TTA	TGT	CAG	AAA	TTA	AAG	ATA	CCA	GAT	CAT	GTC	AGA	GAG	AGA	GCT	TGG	363
Leu	Cys	Gln	Lys	Leu	Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	
	60				65					70				75		
TTA	ACT	TGG	GAG	AAA	GTT	TCA	TCT	GTG	GAT	GGA	GTA	TTG	GGA	GGT	TAT	411
Leu	Thr	Trp	Glu	Lys	Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	
				80					85					90		

33	ATT	CAA	AAG	AAA	AAG	GAA	CTG	TGG	GGA	ATC	TGT	ATC	TTT	ATT	GCA	GCA	459
34	Ile	Gln	Lys	Lys	Lys	Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	
35				95					100					105			
36																	
37	GTT	GAC	CTA	GAT	GAG	ATG	TCG	TTC	ACT	TTT	ACT	GAG	CTA	CAG	AAA	AAC	507
38	Val	Asp	Leu	Asp	Glu	Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	
39			110					115					120				
40																	
41	ATA	GAA	ATC	AGT	GTC	CAT	AAA	TTC	TTT	AAC	TTA	CTA	AAA	GAA	ATT	GAT	555
42	Ile	Glu	Ile	Ser	Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	
43		125					130					135					
44																	
45	ACC	AGT	ACC	AAA	GTT	GAT	AAT	GCT	ATG	TCA	AGA	CTG	TTG	AAG	AAG	TAT	603
46	Thr	Ser	Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	
47	140					145					150					155	
48																	
49	GAT	GTA	TTG	TTT	GCA	CTC	TTC	AGC	AAA	TTG	GAA	AGG	ACA	TGT	GAA	CTT	651
50	Asp	Val	Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	
51					160					165					170		
52																	
53	ATA	TAT	TTG	ACA	CAA	CCC	AGC	AGT	TCG	ATA	TCT	ACT	GAA	ATA	AAT	TCT	699
54	Ile	Tyr	Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	
55				175					180					185			
56																	
57	GCA	TTG	GTG	CTA	AAA	GTT	TCT	TGG	ATC	ACA	TTT	TTA	TTA	GCT	AAA	GGG	747
58	Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	
59			190					195					200				
60																	
61	GAA	GTA	TTA	CAA	ATG	GAA	GAT	GAT	CTG	GTG	ATT	TCA	TTT	CAG	TTA	ATG	795
62	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	
63		205					210				215						
64	CTA	TGT	GTC	CTT	GAC	TAT	TTT	ATT	AAA	CTC	TCA	CCT	CCC	ATG	TTG	CTC	843
65	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	
66	220				225					230					235		
67																	
68	AAA	GAA	CCA	TAT	AAA	ACA	GCT	GTT	ATA	CCC	ATT	AAT	GGT	TCA	CCT	CGA	891
69	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	
70					240					245					250		
71																	
72	ACA	CCC	AGG	CGA	GGT	CAG	AAC	AGG	AGT	GCA	CGG	ATA	GCA	AAA	CAA	CTA	939
73	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	
74				255					260					265			
75																	
76	GAA	AAT	GAT	ACA	AGA	ATT	ATT	GAA	GTT	CTC	TGT	AAA	GAA	CAT	GAA	TGT	987
77	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	
78			270					275					280				
79																	
80	AAT	ATA	GAT	GAG	GTG	AAA	AAT	GTT	TAT	TTC	AAA	AAT	TTT	ATA	CCT	TTT	1035
81	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	
82		285					290					295					
83																	
84	ATG	AAT	TCT	CTT	GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT	CCA	GAG	GTT	GAA	1083
85	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	
86	300				305						310				315		
87																	
88	AAT	CTT	TCT	AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	1131
89	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	
90					320					325					330		
91																	
92	GAT	GCA	AGA	TTA	TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT	CAG	ACT	GAT	TCT	1179
93	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	

94				335				340				345					
95																	
96	ATA	GAC	AGT	TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	1227
97	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	
98				350				355					360				
99																	
100	GAA	GAG	GTG	AAT	GTA	ATT	CCT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	1275
101	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	
102				365				370					375				
103																	
104	AAC	ACT	ATC	CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	1323
105	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	
106	380					385					390					395	
107																	
108	CCT	TCA	GAA	AAT	CTG	ATT	TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	1371
109	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	
110					400					405					410		
111																	
112	AAA	GAA	AGT	ATA	CTG	AAA	AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	1419
113	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	
114				415					420					425			
115																	
116	GAG	AAA	TTT	GCT	AAA	GCT	GTG	GGA	CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	1467
117	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	
118				430				435					440				
119																	
120	CAG	CGA	TAC	AAA	CTT	GGA	GTT	CGC	TTG	TAT	TAC	CGA	GTA	ATG	GAA	TCC	1515
121	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	
122				445				450					455				
123																	
124	ATG	CTT	AAA	TCA	GAA	GAA	GAA	CGA	TTA	TCC	ATT	CAA	AAT	TTT	AGC	AAA	1563
125	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	
126	460					465					470					475	
127																	
128	CTT	CTG	AAT	GAC	AAC	ATT	TTT	CAT	ATG	TCT	TTA	TTG	GCG	TGC	GCT	CTT	1611
129	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	
130					480					485					490		
131																	
132	GAG	GTT	GTA	ATG	GCC	ACA	TAT	AGC	AGA	AGT	ACA	TCT	CAG	AAT	CTT	GAT	1659
133	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	
134				495					500					505			
135																	
136	TCT	GGA	ACA	GAT	TTG	TCT	TTC	CCA	TGG	ATT	CTG	AAT	GTG	CTT	AAT	TTA	1707
137	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	
138				510				515					520				
139																	
140	AAA	GCC	TTT	GAT	TTT	TAC	AAA	GTG	ATC	GAA	AGT	TTT	ATC	AAA	GCA	GAA	1755
141	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	
142				525				530					535				
143																	
144	GGC	AAC	TTG	ACA	AGA	GAA	ATG	ATA	AAA	CAT	TTA	GAA	CGA	TGT	GAA	CAT	1803
145	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	
146	540					545					550					555	
147																	
148	CGA	ATC	ATG	GAA	TCC	CTT	GCA	TGG	CTC	TCA	GAT	TCA	CCT	TTA	TTT	GAT	1851
149	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	
150					560					565					570		
151																	
152	CTT	ATT	AAA	CAA	TCA	AAG	GAC	CGA	GAA	GGA	CCA	ACT	GAT	CAC	CTT	GAA	1899
153	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	
154				575					580					585			



155																	
156	TCT	GCT	TGT	CCT	CTT	AAT	CTT	CCT	CTC	CAG	AAT	AAT	CAC	ACT	GCA	GCA	1947
157	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	
158			590					595					600				
159																	
160	GAT	ATG	TAT	CTT	TCT	CCT	GTA	AGA	TCT	CCA	AAG	AAA	AAA	GGT	TCA	ACT	1995
161	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	
162		605					610					615					
163																	
164	ACG	CGT	GTA	AAT	TCT	ACT	GCA	AAT	GCA	GAG	ACA	CAA	GCA	ACC	TCA	GCC	2043
165	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	
166	620					625					630					635	
167																	
168	TTC	CAG	ACC	CAG	AAG	CCA	TTG	AAA	TCT	ACC	TCT	CTT	TCA	CTG	TTT	TAT	2091
169	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	
170					640					645					650		
171																	
172	AAA	AAA	GTG	TAT	CGG	CTA	GCC	TAT	CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	2139
173	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	
174				655				660						665			
175																	
176	CGC	CTT	CTG	TCT	GAG	CAC	CCA	GAA	TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	2187
177	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	
178			670					675					680				
179																	
180	TTC	CAG	CAC	ACC	CTG	CAG	AAT	GAG	TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	2235
181	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	
182		685					690					695					
183																	
184	TTG	GAC	CAA	ATT	ATG	ATG	TGT	TCC	ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	2283
185	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	
186	700					705					710					715	
187																	
188	AAT	ATA	GAC	CTT	AAA	TTC	AAA	ATC	ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	2331
189	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	
190					720					725					730		
191																	
192	CCT	CAT	GCT	GTT	CAG	GAG	ACA	TTC	AAA	CGT	GTT	TTG	ATC	AAA	GAA	GAG	2379
193	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	
194				735					740					745			
195																	
196	GAG	TAT	GAT	TCT	ATT	ATA	GTA	TTC	TAT	AAC	TCG	GTC	TTC	ATG	CAG	AGA	2427
197	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	
198			750					755					760				
199																	
200	CTG	AAA	ACA	AAT	ATT	TTG	CAG	TAT	GCT	TCC	ACC	AGG	CCC	CCT	ACC	TTG	2475
201	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	
202		765					770					775					
203																	
204	TCA	CCA	ATA	CCT	CAC	ATT	CCT	CGA	AGC	CCT	TAC	AAG	TTT	CCT	AGT	TCA	2523
205	Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	
206	780					785					790					795	
207																	
208	CCC	TTA	CGG	ATT	CCT	GGA	GGG	AAC	ATC	TAT	ATT	TCA	CCC	CTG	AAG	AGT	2571
209	Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	
210					800					805					810		
211																	
212	CCA	TAT	AAA	ATT	TCA	GAA	GGT	CTG	CCA	ACA	CCA	ACA	AAA	ATG	ACT	CCA	2619
213	Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	
214					815				820					825			
215																	

216	AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG	2667
217	Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu	
218	830 835 840	
219		
220	AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC	2715
221	Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu	
222	845 850 855	
223		
224	AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA	2763
225	Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu	
226	860 865 870 875	
227		
228	CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC	2811
229	Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu	
230	880 885 890	
231		
232	CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT	2859
233	Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr	
234	895 900 905	
235		
236	CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA	2907
237	Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser	
238	910 915 920	
239		
240	AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT	2962
241	Asn Lys Glu Glu Lys	
242	925	
243		
244	GGATTCATTG TCTCTCACAG ATGTGACTGT AT	2994

1 36. A pharmaceutical composition of claim 32, wherein said RB cDNA  
2 fragment is selected from the group consisting of RB-1, RB-2, RB-5, y79R8 and mixtures  
3 thereof.

1 37. A pharmaceutical composition of claim 32, wherein a resulting mRNA  
2 transcript of said RB cDNA fragment has 4.6 kb.

1 38. A pharmaceutical composition of claim 37, wherein the cloned  
2 genomic DNA has at least 27 exons.

1 39. A pharmaceutical composition of claim 30, wherein the cloned RB  
2 cDNA transcribes into mRNA which translates in protein having an amino acid sequence  
3 comprising:

4	MPPKTPRKTAATAAAAAAAAAEPPAPPPPPPPPEEDPE	( 34 )
5	QDSGPEDLPLVRLEFEETEEPDF TALCQKLKIPDHVRERA	( 74 )
6	WLTWEKVSSVDGVLGGYIQKKKELWGCICIFIAAVDLDEM	( 114 )
7	FTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKK	( 154 )
8	YDVLFALFSKLER TCELIYLTQPSSSISTEINSALVLKVS	( 194 )
9	WITFLLAKGEVLQMEDDLVISFQLNLCVLDYFIKLSPPML	( 234 )
10	LKEPYKTAVIPINGS PRTPRRGQMR SARI AKQLENDTRII	( 274 )
11	EVLCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEV	( 314 )
12	ENLSKRYEEIYLKNKDL DARLFLDHDKTLQ TDSIDSFETQ	( 354 )
13	RTPRKSNLDEEVNVIPHTPVRTVMNTIQQLMMILNSASD	( 394 )
14	QPSENLISYFNNCTVNP KESILKRVKD IGYIFKEKFAKAV	( 434 )
15	GQGCVEIGSQRYKLGVR LYRVMESMLKSEEERLSIQNFS	( 474 )
16	KLLNDNIFHMSLLACALEVVMATYSRST SQNLDSGTDLSF	( 514 )
17	PWILNVNLKAFDFYKVIESFIKAEGNLTREMIKHLERCE	( 554 )
18	HRIMESLAWLSDSPLFDLIKQSKDREGPTDHLESACPLNL	( 594 )
19	PLQNNHTAADMYLSPVRS PKKKGSTTRVNSTANAETQATS	( 634 )
20	AFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHP	( 674 )
21	ELEHI IWTLFQHTLQNEYELMRDRHLDQIMMCSMYGICKV	( 714 )
22	KNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEEYDSIIV	( 754 )
23	FYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPS	( 794 )
24	SPLRIPGGNIYISPLKSPYKISEGLPTPTKMTPRSRI LVS	( 834 )
25	IGESFGTSEKFQKINQMVCNSDRVLKRSAEGSNPPKPLKK	( 874 )
26	LRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ	( 914 )
27	KMND SMDTSNKEEK	( 928 )

30 single-letter abbreviations for the amino acid residues are:  
31 A, Ala; C, Cys; D, Asp; E, Gly; F, Phe; G, Gly; H, His;  
32 I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln;  
33 R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.

40. A DNA nucleotide sequence comprising:

3	TTCCGGT	TTTT	TCTCAGG	GGA	CGTTGAA	AATT	ATTTT	TGTAA	CGGGAGT	CGG	GAGAGG	ACGG					60
4																	
5	GGCGT	GCCCC	GCGTG	CGCGC	GCGTC	GTCT	CCCCG	GCGCT	CCTCC	ACAGC	TCGCT	GGCTC					120
6																	
7	CCGCC	GCGGA	AAGGC	GTC	ATG	CCG	CCC	AAA	ACC	CCC	CGA	AAA	ACG	GCC	GCC		171
8						Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	
9						1				5					10		
10																	
11	ACC	GCC	GCC	GCT	GCC	GCC	GCG	GAA	CCC	CCG	GCA	CCG	CCG	CCG	CCG	CCC	219
12	Thr	Ala	Ala	Ala	Ala	Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	
13				15					20					25			
14																	
15	CCT	CCG	TAG	GAG	GAC	CCA	GAG	CAG	GAC	AGC	GGC	CCG	GAG	GAC	CTG	CCT	267
16	Pro	Pro	Glu	Glu	Asp	Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	
17			30					35					40				
18																	
19	CTC	GTC	AGG	CTT	GAG	TTT	GAA	GAA	ACA	GAA	GAA	CCT	GAT	TTT	ACT	GCA	315
20	Leu	Val	Arg	Leu	Glu	Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	
21		45					50					55					
22																	
23	TTA	TGT	CAG	AAA	TTA	AAG	ATA	CCA	GAT	CAT	GTC	AGA	GAG	AGA	GCT	TGG	363

24	Leu	Cys	Gln	Lys	Leu	Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	
25	60					65					70					75	
26																	
27	TTA	ACT	TGG	GAG	AAA	GTT	TCA	TCT	GTG	GAT	GGA	GTA	TTG	GGA	GGT	TAT	411
28	Leu	Thr	Trp	Glu	Lys	Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	
29					80					85					90		
30																	
31	ATT	CAA	AAG	AAA	AAG	GAA	CTG	TGG	GGA	ATC	TGT	ATC	TTT	ATT	GCA	GCA	459
32	Ile	Gln	Lys	Lys	Lys	Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	
33				95					100						105		
34																	
35	GTT	GAC	CTA	GAT	GAG	ATG	TCG	TTC	ACT	TTT	ACT	GAG	CTA	CAG	AAA	AAC	507
36	Val	Asp	Leu	Asp	Glu	Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	
37			110					115					120				
38																	
39	ATA	GAA	ATC	AGT	GTC	CAT	AAA	TTC	TTT	AAC	TTA	CTA	AAA	GAA	ATT	GAT	555
40	Ile	Glu	Ile	Ser	Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	
41		125					130					135					
42																	
43	ACC	AGT	ACC	AAA	GTT	GAT	AAT	GCT	ATG	TCA	AGA	CTG	TTG	AAG	AAG	TAT	603
44	Thr	Ser	Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	
45	140					145					150					155	
46																	
47	GAT	GTA	TTG	TTT	GCA	CTC	TTC	AGC	AAA	TTG	GAA	AGG	ACA	TGT	GAA	CTT	651
48	Asp	Val	Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	
49					160					165					170		
50																	
51	ATA	TAT	TTG	ACA	CAA	CCC	AGC	AGT	TCG	ATA	TCT	ACT	GAA	ATA	AAT	TCT	699
52	Ile	Tyr	Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	
53				175					180					185			
54																	
55	GCA	TTG	GTG	CTA	AAA	GTT	TCT	TGG	ATC	ACA	TTT	TTA	TTA	GCT	AAA	GGG	747
56	Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	
57			190					195					200				
58																	
59	GAA	GTA	TTA	CAA	ATG	GAA	GAT	GAT	CTG	GTG	ATT	TCA	TTT	CAG	TTA	ATG	795
60	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	
61		205					210					215					
62	CTA	TGT	GTC	CTT	GAC	TAT	TTT	ATT	AAA	CTC	TCA	CCT	CCC	ATG	TTG	CTC	843
63	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	
64	220				225					230					235		
65																	
66	AAA	GAA	CCA	TAT	AAA	ACA	GCT	GTT	ATA	CCC	ATT	AAT	GGT	TCA	CCT	CGA	891
67	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	
68				240					245						250		
69																	
70	ACA	CCC	AGG	CGA	GGT	CAG	AAC	AGG	AGT	GCA	CGG	ATA	GCA	AAA	CAA	CTA	939
71	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	
72				255					260					265			
73																	
74	GAA	AAT	GAT	ACA	AGA	ATT	ATT	GAA	GTT	CTC	TGT	AAA	GAA	CAT	GAA	TGT	987
75	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	
76			270					275					280				
77																	
78	AAT	ATA	GAT	GAG	GTG	AAA	AAT	GTT	TAT	TTC	AAA	AAT	TTT	ATA	CCT	TTT	1035
79	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	
80		285					290					295					
81																	
82	ATG	AAT	TCT	CTT	GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT	CCA	GAG	GTT	GAA	1083
83	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	
84	300					305					310					315	

85																	
86	AAT	CTT	TCT	AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	1131
87	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	
88					320					325					330		
89																	
90	GAT	GCA	AGA	TTA	TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT	CAG	ACT	GAT	TCT	1179
91	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	
92				335					340					345			
93																	
94	ATA	GAC	AGT	TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	1227
95	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	
96			350					355					360				
97																	
98	GAA	GAG	GTG	AAT	GTA	ATT	CCT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	1275
99	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	
100		365					370					375					
101																	
102	AAC	ACT	ATC	CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	1323
103	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	
104	380					385					390					395	
105																	
106	CCT	TCA	GAA	AAT	CTG	ATT	TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	1371
107	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	
108					400					405					410		
109																	
110	AAA	GAA	AGT	ATA	CTG	AAA	AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	1419
111	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	
112				415					420					425			
113																	
114	GAG	AAA	TTT	GCT	AAA	GCT	GTG	GGA	CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	1467
115	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	
116			430					435					440				
117																	
118	CAG	CGA	TAC	AAA	CTT	GGA	GTT	CGC	TTG	TAT	TAC	CGA	GTA	ATG	GAA	TCC	1515
119	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	
120		445					450					455					
121																	
122	ATG	CTT	AAA	TCA	GAA	GAA	GAA	CGA	TTA	TCC	ATT	CAA	AAT	TTT	AGC	AAA	1563
123	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	
124	460					465					470					475	
125																	
126	CTT	CTG	AAT	GAC	AAC	ATT	TTT	CAT	ATG	TCT	TTA	TTG	GCG	TGC	GCT	CTT	1611
127	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	
128					480					485					490		
129																	
130	GAG	GTT	GTA	ATG	GCC	ACA	TAT	AGC	AGA	AGT	ACA	TCT	CAG	AAT	CTT	GAT	1659
131	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	
132				495					500					505			
133																	
134	TCT	GGA	ACA	GAT	TTG	TCT	TTC	CCA	TGG	ATT	CTG	AAT	GTG	CTT	AAT	TTA	1707
135	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	
136			510					515					520				
137																	
138	AAA	GCC	TTT	GAT	TTT	TAC	AAA	GTG	ATC	GAA	AGT	TTT	ATC	AAA	GCA	GAA	1755
139	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	
140		525					530					535					
141																	
142	GGC	AAC	TTG	ACA	AGA	GAA	ATG	ATA	AAA	CAT	TTA	GAA	CGA	TGT	GAA	CAT	1803
143	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	
144	540					545					550					555	
145																	

146	CGA	ATC	ATG	GAA	TCC	CTT	GCA	TGG	CTC	TCA	GAT	TCA	CCT	TTA	TTT	GAT	1851
147	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	
148					560					565						570	
149																	
150	CTT	ATT	AAA	CAA	TCA	AAG	GAC	CGA	GAA	GGA	CCA	ACT	GAT	CAC	CTT	GAA	1899
151	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	
152				575					580					585			
153																	
154	TCT	GCT	TGT	CCT	CTT	AAT	CTT	CCT	CTC	CAG	AAT	AAT	CAC	ACT	GCA	GCA	1947
155	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	
156			590					595					600				
157																	
158	GAT	ATG	TAT	CTT	TCT	CCT	GTA	AGA	TCT	CCA	AAG	AAA	AAA	GGT	TCA	ACT	1995
159	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	
160		605					610					615					
161																	
162	ACG	CGT	GTA	AAT	TCT	ACT	GCA	AAT	GCA	GAG	ACA	CAA	GCA	ACC	TCA	GCC	2043
163	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	
164	620					625					630					635	
165																	
166	TTC	CAG	ACC	CAG	AAG	CCA	TTG	AAA	TCT	ACC	TCT	CTT	TCA	CTG	TTT	TAT	2091
167	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	
168					640					645					650		
169																	
170	AAA	AAA	GTG	TAT	CGG	CTA	GCC	TAT	CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	2139
171	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	
172				655					660					665			
173																	
174	CGC	CTT	CTG	TCT	GAG	CAC	CCA	GAA	TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	2187
175	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	
176			670					675					680				
177																	
178	TTC	CAG	CAC	ACC	CTG	CAG	AAT	GAG	TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	2235
179	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	
180		685					690					695					
181																	
182	TTG	GAC	CAA	ATT	ATG	ATG	TGT	TCC	ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	2283
183	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	
184	700					705					710					715	
185																	
186	AAT	ATA	GAC	CTT	AAA	TTC	AAA	ATC	ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	2331
187	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	
188					720					725					730		
189																	
190	CCT	CAT	GCT	GTT	CAG	GAG	ACA	TTC	AAA	CGT	GTT	TTG	ATC	AAA	GAA	GAG	2379
191	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	
192				735					740					745			
193																	
194	GAG	TAT	GAT	TCT	ATT	ATA	GTA	TTC	TAT	AAC	TCG	GTC	TTC	ATG	CAG	AGA	2427
195	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	
196			750					755					760				
197																	
198	CTG	AAA	ACA	AAT	ATT	TTG	CAG	TAT	GCT	TCC	ACC	AGG	CCC	CCT	ACC	TTG	2475
199	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	
200		765					770					775					
201																	
202	TCA	CCA	ATA	CCT	CAC	ATT	CCT	CGA	AGC	CCT	TAC	AAG	TTT	CCT	AGT	TCA	2523
203	Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	
204	780					785					790					795	
205																	
206	CCC	TTA	CGG	ATT	CCT	GGA	GGG	AAC	ATC	TAT	ATT	TCA	CCC	CTG	AAG	AGT	2571

207 Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser  
 208 800 805 810  
 209  
 210 CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA 2619  
 211 Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro  
 212 815 820 825  
 213  
 214 AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG 2667  
 215 Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu  
 216 830 835 840  
 217  
 218 AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC 2715  
 219 Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu  
 220 845 850 855  
 221  
 222 AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA 2763  
 223 Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu  
 224 860 865 870 875  
 225  
 226 CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC 2811  
 227 Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu  
 228 880 885 890  
 229  
 230 CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT 2859  
 231 Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr  
 232 895 900 905  
 233  
 234 CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA 2907  
 235 Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser  
 236 910 915 920  
 237  
 238 AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT 2962  
 239 Asn Lys Glu Glu Lys  
 240 925  
 241  
 242 GGATTCATTG TCTCTCACAG ATGTGACTGT AT 2994

1 41. A method of therapeutically treating inactive, mutative or absent  
 2 cancer suppressing genes comprising:  
 3 treating said inactive, mutative or absent cancer suppressing genes with at  
 4 least a portion of intact cancer suppressing genes.

1 42. A method of claim 41, wherein said cancer suppressing genes are each  
 2 a substance selected from the groups consisting of RB genes, breast cancer suppressing  
 3 genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes,  
 4 bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes,  
 5 small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes,  
 6 acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, and mixtures  
 7 thereof.

1 43. A method of claim 41, wherein said treating includes:

2           treating said inactive, mutative or absent cancer suppressing gene with a  
3 substance selected from the group consisting of an RB gene, a portion of said gene, or a  
4 mixture thereof.

1           44.     A method of claim 43, wherein said portion is selected from the group  
2 consisting of RB cDNA, RB cDNA fragment, homologues thereof and mixtures thereof.

1           45.     The method of claim 41, wherein the intact cancer suppressing gene, or  
2 portion thereof, is delivered to the site of a tumor by means of a retrovirus.

1           46.     A method of claim 41, wherein the intact cancer suppressing gene, or a  
2 portion thereof, is delivered to the site of a tumor by a liposome.

1           47.     A method of claim 41, wherein the location of said cancer suppressing  
2 gene is determined by utilizing a genetic marker.